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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/763,992

DATE: 02/10/2004

TIME: 10:10:47

Input Set : N:\CrF3\RULE60\10763992.RAW.txt

Output Set: N:\CRF4\02102004\J763992.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

4 (i) APPLICANT: COHEN, Maurice
 5 FRIEDMAN, Paula N.
 6 GORDON, Julian
 7 HODGES, Steven C.
 8 KLASS, Michael R.
 9 KRATOCHVIL, Jon D.
 10 ROBERTS-RAPP, Lisa
 11 RUSSELL, John C.
 12 STROUPE, Steven D.

13 (ii) TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
 14 FOR DETECTING DISEASES OF THE PROSTATE

15 (iii) NUMBER OF SEQUENCES: 35

16 (iv) CORRESPONDENCE ADDRESS:
 17 (A) ADDRESSEE: Abbott Laboratories
 18 (B) STREET: 100 Abbott Park Road
 19 (C) CITY: Abbott Park
 20 (D) STATE: IL
 21 (E) COUNTRY: USA
 22 (F) ZIP: 60064-3500

23 (v) COMPUTER READABLE FORM:
 24 (A) MEDIUM TYPE: Diskette
 25 (B) COMPUTER: IBM Compatible
 26 (C) OPERATING SYSTEM: DOS
 27 (D) SOFTWARE: FastSEQ for Windows Version 2.0

28 (vi) CURRENT APPLICATION DATA:
 29 (A) APPLICATION NUMBER: US/10/763,992

C--> 30 (B) FILING DATE: 22-Jan-2004
 31 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:
 33 (A) APPLICATION NUMBER: US/09/418,887
 34 (B) FILING DATE: 15-OCT-1999
 36 (A) APPLICATION NUMBER: US/08/946,869
 37 (B) FILING DATE: 08-Oct-1997

38 (viii) ATTORNEY/AGENT INFORMATION:
 39 (A) NAME: Becker, Cheryl L.
 40 (B) REGISTRATION NUMBER: 35,441
 41 (C) REFERENCE/DOCKET NUMBER: 5697.US.P1

42 (ix) TELECOMMUNICATION INFORMATION:
 43 (A) TELEPHONE: 847/935-1729
 44 (B) TELEFAX: 847/938-2623
 45 (C) TELEX:

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46 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

- 48 (A) LENGTH: 367 base pairs
- 49 (B) TYPE: nucleic acid
- 50 (C) STRANDEDNESS: single
- 51 (D) TOPOLOGY: linear

52 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

53 TGC	GCNGGAG	CCTGAGCGGA	GGGTGTGCGC	AGCCTCGCCA	GCGGGGGCCC	CGGGCTGN	60
54 CATTG	CCTCA	CTGAGCCAGC	GCCTGCCTNC	TACCTCGCCG	ACAGCTGGAA	CCAGTGC	120
55 CTAGT	GGGCTC	TCACCTGCTT	CCTCCTGGC	GTGGGCTGCC	GGCTGACCCC	GGGTTTGT	180
56 CACCT	GGGCC	GCAC	TCATCGAC	TTCATGGTT	TCACGGTGCG	GCTGCTTCAC	240
57 ATCTT	CACGG	TCAACAAACA	GCTGGGGCCC	AAGATCGTCA	TCGTGAGCAA	GATGATGAAG	300
58 GACGT	GTTCT	TCTTCCTCTT	CTTCCTCGGC	GTGTGGCTGG	TAGCTATGGG	TTGGGCCACG	360
59 GAGGGGT							367

61 (2) INFORMATION FOR SEQ ID NO: 2:

62 (i) SEQUENCE CHARACTERISTICS:

- 63 (A) LENGTH: 214 base pairs
- 64 (B) TYPE: nucleic acid
- 65 (C) STRANDEDNESS: single
- 66 (D) TOPOLOGY: linear

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

68 CAAAC	AAGCTG	GGGCCAAAGA	TCGTCATCGT	GAGCAAGATG	ATGAAGGACG	TGTTCTTCTT	60
69 CCTCTT	CTTC	CTCGCGTGT	GGCTGGTAGC	CTATGGCGTG	GCCACGGAGG	GGCTCCTGAG	120
70 GCCAC	GGGAC	AGTGA	CTTCC	CAAGTATCCT	GCGCCGCGTC	TTCTACCGTC	180
71 GATCTTC	GGG	CAGATT	CCCC	AGGAGGACAT	GGAC		214

73 (2) INFORMATION FOR SEQ ID NO: 3:

74 (i) SEQUENCE CHARACTERISTICS:

- 75 (A) LENGTH: 205 base pairs
- 76 (B) TYPE: nucleic acid
- 77 (C) STRANDEDNESS: single
- 78 (D) TOPOLOGY: linear

79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

80 CGTGTGGCTG	GTAGCCTATG	GCGTGGCCAC	GGAGGGCTC	CTGAGGCCAC	GGGACAGTGA		60
81 CTTCCAAGT	ATCCTGCGCC	GCGTCTTCTA	CCGTCCTAC	CTGCAGATCT	TCGGGCAGAT		120
82 TCCCCAGGAG	GACATGGACG	TGGCCCTCAT	GGAGCACAGC	AACTGCTCGT	CGGAGCCCGG		180
83 CTTCTGGGCA	CACCC	CTCTG	GGGCC				205

85 (2) INFORMATION FOR SEQ ID NO: 4:

86 (i) SEQUENCE CHARACTERISTICS:

- 87 (A) LENGTH: 256 base pairs
- 88 (B) TYPE: nucleic acid
- 89 (C) STRANDEDNESS: single
- 90 (D) TOPOLOGY: linear

91 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

92 CGGGCAGATT	CCCCAGGAGG	ACATGGACGT	GGCCCTCATG	GAGCACAGCA	ACTGCTCGTC		60
93 GGAGCCCGGC	TTCTGGGCAC	ACCCTCCTGG	GGCCCAGGCG	GGCACCTGCG	TCTCCCAGTA		120
94 TGCCA	ACTGG	CTGGTGGTGC	TGCTCCTCGT	CATCTCCTG	CTCGTGGCCA	ACATCCTGCT	180
95 GGTCA	ACTTG	CTCATTGCCA	TGTCAGTTA	CACATT	CGGC	AAAGTACAGG	240
96 TCTCT	ACTGG	AAGGCG					256

98 (2) INFORMATION FOR SEQ ID NO: 5:

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99 (i) SEQUENCE CHARACTERISTICS:
 100 (A) LENGTH: 246 base pairs
 101 (B) TYPE: nucleic acid
 102 (C) STRANDEDNESS: single
 103 (D) TOPOLOGY: linear
 104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 105 GCGATCTCTA CTGGAAGGCG CAGGTTACCG CCTCATCCGG GAATTCCACT CTCGGCCCGC 60
 106 GCTGGCCCCG CCCTTATCG TCATCTCCA CTTGCGCCTC CTGCTCAGGC AATTGTGCAG 120
 107 GCGACCCCGG AGCCCCCAGC CGTCCTCCCC GGCCTCGAG CATTCCGGG TTTACCTTTC 180
 108 TAAGGAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG CATAAGGAGA ACTTTCTGCT 240
 109 GGCACG 246
 111 (2) INFORMATION FOR SEQ ID NO: 6:
 112 (i) SEQUENCE CHARACTERISTICS:
 113 (A) LENGTH: 277 base pairs
 114 (B) TYPE: nucleic acid
 115 (C) STRANDEDNESS: single
 116 (D) TOPOLOGY: linear
 117 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 118 GTGCATAAGG AGAACTTTCT GCTGGCACCG GCTAGGGACA AGCGGGAGAG CGACTCCGAG 60
 119 CGTCTGAAGC GCACGTCCA GAAGGGTGGAC TTGGCACTGA AACAGCTGGG ACACATCCGC 120
 120 GAGTACGAAC AGCGCCTGAA AGTGTGGAG CGGGAGGTCC AGCAGTGTAG CCGCGTCCTG 180
 121 GGGTGGGTGG CCGAGGCCCT GAGCCGCTCT GCCTTGCTGC CCCCAGGTGG GCCGCCACCC 240
 122 CCTGACCTGC CTGGGTCCAA AGACTGAGCC CTGCTGG 277
 124 (2) INFORMATION FOR SEQ ID NO: 7:
 125 (i) SEQUENCE CHARACTERISTICS:
 126 (A) LENGTH: 251 base pairs
 127 (B) TYPE: nucleic acid
 128 (C) STRANDEDNESS: single
 129 (D) TOPOLOGY: linear
 130 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 131 GGGTCCAAAG ACTGANCCCT GCTGGCGGAC TTCAAGGAGA AGCCCCCACA GGGGATTTTG 60
 132 CTCCTAGAGT AAGGCTCATC TGGGCCTCGG CCCCCGCACC TGGTGGCCTT GTCCTTGAGG 120
 133 TGAGCCCCAT GTCCATCTGG GCCACTGTCA GGACCACCTT TGGGAGTGTCA ATCCTTACAA 180
 134 ACCACAGCAT GCCCGGCTCC TCCCAGAACC AGTCCCAGCC TGGGAGGATC AAGGCCTGGA 240
 135 TCCCAGGCCG T 251
 137 (2) INFORMATION FOR SEQ ID NO: 8:
 138 (i) SEQUENCE CHARACTERISTICS:
 139 (A) LENGTH: 223 base pairs
 140 (B) TYPE: nucleic acid
 141 (C) STRANDEDNESS: single
 142 (D) TOPOLOGY: linear
 143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 144 GGCTCATCTG GGCCTCGGCC CCCGCACCTG GTGGCCTTGT CCTTGAGGTG AGCCCCATGT 60
 145 CCATCTGGGC CACTGTCAAG ACCACCTTTG GGAGTGTCA CTTACAAAC CACAGCATGC 120
 146 CCGGCTCCTC CCAGAACAG TCCCAGCCTG GGAGGATCAA GGCCTGGATC CCGGGCCGTT 180
 147 ATCCATCTGG AGGCTGCAGG GTCCTGGGG TAACAGGGAC CAC 223
 149 (2) INFORMATION FOR SEQ ID NO: 9:
 150 (i) SEQUENCE CHARACTERISTICS:
 151 (A) LENGTH: 2393 base pairs

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152 (B) TYPE: nucleic acid
 153 (C) STRANDEDNESS: single
 154 (D) TOPOLOGY: linear
 155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 156 AAGGCCACCT CGCCGCTCTC CTGGATGCTG GCCTCGGCAG GCCCCCTGAA CCTGCTTCTT 60
 157 TGGGCACTGT TGCTGAAACA GGCACAGATG GCCATGTACT TCTGGGAGAT GGGTTCCAAT 120
 158 GCAGTTTCT CAGCTCTTGG GGCCTGTTG CTGCTCCGGG TGATGGCAGC CCTGGAGCCT 180
 159 GACGCTGAGG AGGCAGCACG GAGGAAGAC CTGGCGTTCA AGTTGAGGG GATGGGCGTT 240
 160 GACCTCTTTG GCGAGTGCTA TCGCAGCAGT GAGGTGAGGG CTGCCCGCCT CCTCCTCCGT 300
 161 CGYTGCCCGC TCTGGGGGGA TGCCACTTTG CCTTCCAGGT GGCCATGCAA AGCTGACGSC 360
 162 CSTGMCTTCT TTGCCMAGGA TGGGGTACAG TCTCTGCTGA CACAGAAGTG GTGGGGAGAT 420
 163 ATGGCCAGCA CTACACCCAT CTGGGCCCTG GTTATCGCGT TCTTTGCCCT TCCACTCATC 480
 164 TACACCCGCC TCATCACCTT CAGGAATCA GAAGAGGAGC CCACACGGGA GGAGCTAGAG 540
 165 TTTGACATGG ATAGTGTCTA TAATGGGAA GGGCCTGTCG GGACGGCGGA CCCAGCCGAG 600
 166 AAGACGCCGC TGGGGGTCCC GCGCCAGTCG GGGCGTCCGG GTTGCTGCGG GGGCGCTGC 660
 167 GGGGGCGGCC GGTGCCTACG CCGCTGGTTC CACTCTGGG GCGCGCCGGT GACCATCTTC 720
 168 ATGGGCAACG TGGTCAGCTA CCTGCTGTTG CTGCTGCTTT TCTCGCGGGT GCTGCTCGT 780
 169 GATTTCAGC CGGCGCCCGC CGGCTCCCTG GAGCTGCTGC TCTATTCTG GGCTTTCACG 840
 170 CTGCTGTGCG AGGAATGCGC CAGGGCCTGA GCGGAGGCGG GGGCAGCCTC GCCAGCGGG 900
 171 GCCCCGGGCC TGGCCATGCC TCACTGAGCC AGCGCCTGCG CCTCTACCTC GCCGACAGCT 960
 172 GGAACCAAGT CGACCTAGTG GCTCTCACCT GCTTCCTCCT GGGCGTGGGC TGCCGGCTGA 1020
 173 CCCCCGGGTTT GTACCACCTG GGCGCAGCTG TCCCTGCTCAT CGACTTCATG GTTTTCACGG 1080
 174 TCGGGCTGCT TCACATCTTC ACGGTCAACA AACAGCTGGG GCCCAAGATC GTCATCGTGA 1140
 175 GCAAGATGAT GAAGGACGTG TTCTTCTTCC TCTTCTTCCT CGGCCTGTTG CTGGTAGCCT 1200
 176 ATGGCGTGGC CACGGAGGGG CTCCCTGAGGC CACGGGACAG TGACTTCCCAGTATCCTGC 1260
 177 GCCCGCTCTT CTACCCTGCC TACCTGAGA TCTTCGGGCA GATTCCCCAG GAGGACATGG 1320
 178 ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG GCACACCCCTC 1380
 179 CTGGGGCCCA GGCGGGCACC TGCCTCTCCC AGTATGCCAA CTGGCTGGTG GTGCTGCTCC 1440
 180 TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAA CTTGCTCATT GCCATGTTCA 1500
 181 GTTACACATT CGGCAAAGTA CAGGGCACA GCGATCTCTA CTGGAAGGCG CAGGTTACCG 1560
 182 CCTCATCCGG GAATTCCACT CTCGGCCCGC GCTGGCCCCG CCCTTATCG TCATCTCCCA 1620
 183 CTTGCGCCTC CTGCTCAGGC AATTGTGCAG GCGACCCCGG AGCCCCCAGC CGTCCTCCCC 1680
 184 GGCCCTCGAG CATTTCCGGG TTTACCTTC TAAGGAAGCC GAGCAGGAAGC TGCTAACGTG 1740
 185 GGAATCGGTG CATAAGGAGA ACTTCTGCT GGCACCGCCT AGGGACAAGC GGGAGAGCGA 1800
 186 CTCCGAGCGT CTGAAGCGCA CGTCCCAGAA GGTGGACTTG GCACTGAAAC AGCTGGGACA 1860
 187 CATCCGCGAG TAGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC AGTGTAGCCG 1920
 188 CGTCCTGGGG TGGGTGGCCG AGGCCCTGAG CGCCTCTGCC TTGCTGCCCT CAGGTGGGCC 1980
 189 GCCACCCCT GACCTGCCCTG GGTCCAAAGA CTGAGCCCTG CTGGCGGACT TCAAGGAGAA 2040
 190 GCCCCCACAG GGGATTTGC TCCTAGAGTA AGGCTCATCT GGGCCTCGGC CCCCGCACCT 2100
 191 GGTGGCCTTG TCCTTGAGGT GAGCCCCATG TCCATCTGGG CCACTGTCAG GACCACCTT 2160
 192 GGGAGTGTCA TCCTTACAAA CCACAGCATG CCCGGCTCCT CCCAGAACCA GTCCCAGCCT 2220
 193 GGGAGGATCA AGCCCTGGAT CCCGGCCGT TATCCATCTG GAGGCTGAG GGTCTTGGG 2280
 194 GTAACAGGGA CCACAGACCC CTCACCACTC ACAGATTCCCT CACACTGGGG AAATAAAGCC 2340
 195 ATTCAGAGG AAAAAAAA AAAAAAAA AAAAAAAA GGGCGGCCGC GGT 2393

197 (2) INFORMATION FOR SEQ ID NO: 10:

198 (i) SEQUENCE CHARACTERISTICS:

199 (A) LENGTH: 1297 base pairs

200 (B) TYPE: nucleic acid

201 (C) STRANDEDNESS: single

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202 (D) TOPOLOGY: linear

203 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

204	GAATTCGGCT CGAGCAAAACA GCTGGGGCCC AAGATCGTCA TCGTGAGCAA GATGATGAAG	60
205	GACGTGTTCT TCTTCCTCTT CTTCCCTCGGC GTGTGGCTGG TAGCCTATGG CGTGGCCACG	120
206	GAGGGGCTCC TGAGGCCACG GGACAGTGAC TTCCCAAGTA TCCTGCGCCG CGTCTTCTAC	180
207	CGTCCCTACC TGCAAGATCTT CGGGCAGATT CCCCAGGAGG ACATGGACGT GGCCCTCATG	240
208	GAGCACAGCA ACTGCTCGTC GGAGCCCGGC TTCTGGGCAC ACCCTCCTGG GGCCCAGGCG	300
209	GGCACCTGCG TCTCCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCCTCGT CATCTTCCTG	360
210	CTCGTGGCCA ACATCCTGCT GGTCAACTTG CTCATTGCCA TGTTCAAGTTA CACATTGGC	420
211	AAAGTACAGG GCAACAGCGA TCTCTACTGG AAGGCGCAGC GTTACCCGCT CATCCGGAA	480
212	TTCCACTCTC GGCCCGCGCT GGCCCCGCC TTATCGTCA TCTCCCACTT GCGCCTCCTG	540
213	CTCAGGCAAT TGTGCAGGCG ACCCCGGAGC CCCCAGCCGT CCTCCCCGGC CCTCGAGCAT	600
214	TTCCGGGTTT ACCTTTCTAA GGAAGCCGAG CGGAAGCTGC TAACGTGGGA ATCGGTGCAT	660
215	AAGGAGAACT TTCTGCTGGC ACGCGCTAGG GACAAGCGGG AGAGCGACTC CGAGCGTCTG	720
216	AAGCGCACGT CCCAGAAGGT GGACTTGGCA CTGAAACAGC TGGGACACAT CGCGAGTAC	780
217	GAACAGCGCC TGAAAAGTGCT GGAGCGGGAG GTCCAGCAGT GTAGCCCGGT CCTGGGGTGG	840
218	GTGGCCGAGG CCCTGAGCCG CTCTGCCTTG CTGCCCCCAG GTGGGCCGCC ACCCCCTGAC	900
219	CTGCCTGGGT CCAAAGACTG AGCCCTGCTG GCGGACTTCA AGGAGAAAGCC CCCACAGGGG	960
220	ATTTTGCTCC TAGAGTAAGG CTCATCTGGG CCTCGGGCCCC CGCACCTGGT GGCCTTGTCC	1020
221	TTGAGGTGAG CCCCATGTCC ATCTGGCCA CTGTCAGGAC CACCTTGGG AGTGTATCC	1080
222	TTACAAACCA CAGCATGCC GGCTCCTCCC AGAACCAAGTC CCAGCCTGGG AGGATCAAGG	1140
223	CCTGGATCCC GGGCCGTTAT CCATCTGGAG GCTGCAGGGT CCTTGGGGTA ACAGGGACCA	1200
224	CAGACCCCTC ACCACTCACA GATTCCCTAC ACTGGGGAAA TAAAGCCATT TCAGAGGAAA	1260
225	AAAAAAAAA AAAAAAAA AAAAAAAGGG CGGCCGC	1297

227 (2) INFORMATION FOR SEQ ID NO: 11:

228 (i) SEQUENCE CHARACTERISTICS:

- 229 (A) LENGTH: 68 base pairs
- 230 (B) TYPE: nucleic acid
- 231 (C) STRANDEDNESS: single
- 232 (D) TOPOLOGY: linear

233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

234	AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC	60
235	CGGGAATT	68

237 (2) INFORMATION FOR SEQ ID NO: 12:

238 (i) SEQUENCE CHARACTERISTICS:

- 239 (A) LENGTH: 68 base pairs
- 240 (B) TYPE: nucleic acid
- 241 (C) STRANDEDNESS: single
- 242 (D) TOPOLOGY: linear

243 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

244	AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCCG CTCTAGAGGA TCCAAGCTCG	60
245	GAATTCCG	68

247 (2) INFORMATION FOR SEQ ID NO: 13:

248 (i) SEQUENCE CHARACTERISTICS:

- 249 (A) LENGTH: 24 base pairs
- 250 (B) TYPE: nucleic acid
- 251 (C) STRANDEDNESS: single
- 252 (D) TOPOLOGY: linear

253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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Input Set : N:\Crf3\RULE 60\10763992.RAW.txt
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 53, 54, 55, 56, 57, 58, 59
Seq#:2; Line(s) 68, 69, 70, 71
Seq#:3; Line(s) 80, 81, 82, 83
Seq#:4; Line(s) 92, 93, 94, 95, 96
Seq#:5; Line(s) 105, 106, 107, 108, 109
Seq#:6; Line(s) 118, 119, 120, 121, 122
Seq#:7; Line(s) 131, 132, 133, 134, 135
Seq#:8; Line(s) 144, 145, 146, 147
Seq#:9; Line(s) 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170
Seq#:9; Line(s) 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185
Seq#:9; Line(s) 186, 187, 188, 189, 190, 191, 192, 193, 194, 195
Seq#:10; Line(s) 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217
Seq#:10; Line(s) 218, 219, 220, 221, 222, 223, 224, 225
Seq#:11; Line(s) 234, 235
Seq#:12; Line(s) 244, 245
Seq#:13; Line(s) 254
Seq#:14; Line(s) 263
Seq#:15; Line(s) 272
Seq#:16; Line(s) 281
Seq#:17; Line(s) 290
Seq#:18; Line(s) 299
Seq#:19; Line(s) 308
Seq#:20; Line(s) 317
Seq#:21; Line(s) 326
Seq#:22; Line(s) 335
Seq#:23; Line(s) 344
Seq#:24; Line(s) 353

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/763,992

DATE: 02/10/2004

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Input Set : N:\Crf3\RULE60\10763992.RAW.txt

Output Set: N:\CRF4\02102004\J763992.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:361 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:454 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:466 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:477 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:488 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:499 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:510 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:521 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:532 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33